```
                  9      18      27      36      45      54
5'  GGG  ACT  TCC  AGT  AGG  AGG  CGG  CAT  GTT  TGA  AAA  GTG  ATG  ACG  GTT  GAC  GTT  TGC
    --   --   --   --   --   --   --   --   --   --   --   --   --   --   --   --   --   --

                 63      72      81      90      99     108
    TGA  TTT  TTG  ACT  TTG  CTT  GTA  GCT  CCC  CGA  ACT  CGC  CGT  CTT  CCT  GTC  GGC
    --   --   --   --   --   --   --   --   --   --   --   --   --   --   --   --   --

                117     126     135     144     153     162
    GGC  CGG  CAC  TGT  AGG  TGA  GCG  CGA  GAG  GAC  GGA  AGG  AAG  CCT  GCA  GAC  AGA
    --   --   --   --   --   --   --   --   --   --   --   --   --   --   --   --   --

                171     180     189     198     207     216
    CGC  CTT  CAT  CCC  AAG  GCG  GCA  GGT  CGG  ACG  GGG  ACG  CTG  GGC  CTG  GCG  GTG
    --   --   --   --   --   --   --   --   --   --   --   --   --   --   --   --   --

                225     234     243     252     261     270
    TTT  TCG  TGC  TCA  GCG  GTG  GGA  GGA  GGC  AGA  AAC  CAG  AGA  AAC  ACG  CTG  GGA  GAT
    --   --   --   --   --   --   --   --   --   --   --   --   --   --   --   --   --   --

                279     288     297     306     315     324
    TAA  CAG  GAA  ACT  TCC  AAG  ATG  GAA  ACT  TTG  TCT  TTC  CCC  AGA  TAT  AAT  GTA  GCT
    --   --   --   --   --         M    E    T    L    S    F    P    R    Y    N    V    A

                333     342     351     360     369     378
    GAG  ATT  GTG  ATT  CAT  ATT  CGC  AAT  AAG  ATC  TTA  ACA  GGA  GCT  GAT  GGT  AAA  AAC
     E    I    V    I    H    I    R    N    K    I    L    T    G    A    D    G    K    N
```

FIGURE 1A

```
            387         396         405         414         423         432
CTC ACC AAG AAT GAT CTT TAT CCA AAG CCT GAA GTC TTG CAC ATG ATC
 L   T   K   N   D   L   Y   P   K   P   E   V   L   H   M   I

        441         450         459         468         477         486
TAC ATG AGA GCC TTA CAA ATA GTA TAT GGA ATT CGA CTG GAA TTT TAC ATG
 Y   M   R   A   L   Q   I   V   Y   G   I   R   L   E   H   F   Y   M

        495         504         513         522         531         540
ATG CCA AAC TCT GAA GTC ATG TAT CCA CAT TTA ATG GAA TTC TTA CCA
 M   P   N   S   E   V   M   Y   P   H   L   M   E   F   L   P

        549         558         567         576         585         594
TTC AGC AAT TTA GTT ACT CAT CTG GAC TCA TTT TTG CCT ATC TGC CGG GTG AAT
 F   S   N   L   V   T   H   L   D   S   F   L   P   I   C   R   V   N

        603         612         621         630         639         648
GAC TTT GAG ACT GCT GAT ATT CTA TGT CCA AAA CGG GCA AAA AGT CGG TTT
 D   F   E   T   A   D   I   L   C   P   K   A   K   R   S   R   F

        657         666         675         684         693         702
TTA AGT GGC ATT ATC AAC TTT ATT CAC TTC AGA GAA GCA TGC CGT GAA ACG TAT
 L   S   G   I   I   N   F   I   H   F   R   E   A   C   R   E   T   Y
```

FIGURE 1B

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

```
                711            720            729            738            747            756
    ATG GAA    TTT    CTT TGG CAA    TAT AAA TCC    TCT GCG GAC    AAA ATG CAA    CAG TTA AAC
  |   |   |  |   |  |   |   |  |   |   |   |  |   |   |   |  |   |   |   |  |   |   |   |  |   |   |
     M   E     F      L   W   Q      Y   K   S      S   A   D      K   M   Q      Q   L   N

                765            774            783            792            801            810
    GCC GCA    CAC    CAG GAG TTA    ATG AAA CTG    GAG AGA CTT    GAT TCT GTT    CCA GTT
  |   |   |  |   |  |   |   |  |   |   |   |  |   |   |   |  |   |   |   |  |   |   |
     A   A     H      Q   E   L      M   K   L      E   R   L      D   S   V      P

                819            828            837            846            855            864
    GAA GAG    CAA    GAA TTC AAG    CAG CTT TCA    GAT GGA ATT    CAG GAG CTA    CAA CAA
  |   |   |  |   |  |   |   |  |   |   |   |  |   |   |   |  |   |   |   |  |   |   |
     E   E     Q      E   F   K      Q   L   S      D   G   I      Q   E   L      Q   Q

                873            882            891            900            909            918
    TCA CTA    AAT    CAG GAT TTT    CAT CAA AAA    ACG ATA GTG    CTG CAA GAG    GGA AAT TCC
  |   |   |  |   |  |   |   |  |   |   |   |  |   |   |   |  |   |   |   |  |   |   |
     S   L     N      Q   D   F      H   Q   K      T   I   V      L   Q   E      G   N   S

                927            936            945            954            963            972
    CAA AAG    TCA    AAT ATT TCA    GAG AAA ACC    AAG CGT TTG    AAT GAA CTA    AAA TTG
  |   |   |  |   |  |   |   |  |   |   |   |  |   |   |   |  |   |   |   |  |   |   |
     Q   K     S      N   I   S      E   K   T      K   R   L      N   E   L      K   L

                981            990            999           1008           1017           1026
    TCG GTG    TCT    TTG AAA GAA    ATA CAA GAG    AGT TTG AAA    ACA AAA ATT    GTG GAT
  |   |   |  |   |  |   |   |  |   |   |   |  |   |   |   |  |   |   |   |  |   |   |
     S   V     S      L   K   E      I   Q   E      S   L   K      T   K   I      V   D
```

FIGURE 1C

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

```
       1035        1044        1053        1062        1071        1080
TCT CCA AAG GAG TTA AAG AAT TAT GAA ATG AAA GAT ACG GTC CAG AAG
---   --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S    P   K   E   L   K   N   Y   E   M   K   D   T   V   Q   K

       1089        1098        1107        1116        1125        1134
CTT AAA AAT GCC AGA CAA GAA GTG GAG AAA TAT GGA GAC TCA
---   --- --- --- --- --- --- --- --- --- --- --- --- ---
 L    K   N   A   R   Q   E   V   E   K   Y   G   D   S

       1143        1152        1161        1170        1179        1188
GTT GAC TGC CTG CCT TCA TGT CAG TTG GAA GTG CAG TTA TAT CAA AAG AAA ATA
---   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V    D   C   L   P   S   C   Q   L   E   V   Q   L   Y   Q   K   K   I

       1197        1206        1215        1224        1233        1242
CAG GAC CTT TCA GAT AAT AGG GAA AAA TTA GCC AGT ATC TTA AAG GAG AGC CTG
---   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q    D   L   S   D   N   R   E   K   L   A   S   I   L   K   E   S   L

       1251        1260        1269        1278        1287        1296
AAC TTG GAG GAC CAA ATT GAG GAT GAG AGT TCA GAA CTG AAG AAA TTG AAG ACT
---   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 N    L   E   D   Q   I   E   D   E   S   S   E   L   K   K   L   K   T

       1305        1314        1323        1332        1341        1350
GAA GAA AAT TCG TTC AAA AGA CTG ATG ATT GTG AAG GAA AAA CTT GCC ACA
---   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E    E   N   S   F   K   R   L   M   I   V   K   E   K   L   A   T
```

FIGURE 1D

```
        1359        1368        1377        1386        1395        1404
        GCA CAA TTC AAA ATA AAT AAG AAG CAT GAA GAT GTT AAG CAA TAC AAA CGC ACA
        A   Q   F   K   I   N   K   K   H   E   D   V   K   Q   Y   K   R   T

        1413        1422        1431        1440        1449        1458
        GTA ATT GAG GAT TGC AAT AAA GTT CAA GAA AAA AGA GGT GCT GTC TAT GAA CGA
        V   I   E   D   C   N   K   V   Q   E   K   R   G   A   V   Y   E   R

        1467        1476        1485        1494        1503        1512
        GTA ACC ACA ATT AAT CAA GAA ATC AAA ATT CTT GGA ATT CAA CAA CTA
        V   T   T   I   N   Q   E   I   K   I   L   G   I   Q   Q   L

        1521        1530        1539        1548        1557        1566
        AAA GAT GCT GCT GAA AGG GAG AAA CTG AAG TCC CAG GAA ATA TTT CTA AAC TTG
        K   D   A   A   E   R   E   K   L   K   S   Q   E   I   F   L   N   L

        1575        1584        1593        1602        1611        1620
        AAA ACT GCT TTG GAG AAA TAC CAC GAC GGT ATT GAA AAG GCA GAG GAC TCC
        K   T   A   L   E   K   Y   H   D   G   I   E   K   A   E   D   S

        1629        1638        1647        1656        1665        1674
        TAT GCT AAG ATA GAT GAG AAG ACA GCT GAA CTG AAG AGG AAG ATG TTC AAA ATG
        Y   A   K   I   D   E   K   T   A   E   L   K   R   K   M   F   K   M
```

FIGURE 1E

FIGURE 1F

```
       1683      1692      1701      1710      1719      1728
TCA ACC TGA TTA  AAA TTA ACA  CAT GTC TTT  TTG TAA ATG  GCT TGC CAT  CTT TTA
        S   T                                                        *

       1737      1746      1755      1764      1773      1782
ATT TTC TAT TTA  GAA AGA AAA  GTT GAA GCG  AAT GGA AGT  ATC AGA AGT  ACC AAA

       1791      1800      1809      1818      1827      1836
TAA TGT TGG CTT  CAT CAG TTT  TTA TAC ACT  CTC ATA AGT  AGT TAA TAA  GAT GAA

       1845      1854      1863      1872      1881      1890
TTT AAT GTA GGC  TTT TAT TAA  TTT ATA ATT  AAA ATA ACT  TGT GCA GCT  ATT CAT

       1899      1908      1917      1926      1935      1944
GTC TCT ACT CTG  CCC CTT GTT  GTA AAT AGT  TTG AGT AAA  ACA AAA CTA  GTT ACG

       1953      1962      1971
TTT GAA ATA TAT  ATA TTT TTT  TCT GTT ACA AAA AA 3'
```

FIGURE 1F

```
  1  M E T L S F P R Y N V A E I V I H I R N K I L T G A D G K N   GRIIP
  1  M E T L S F P R Y N I A E I V V H I R N K L L T G A D G K N   HW051

 31  L T K N D L Y P N P K P E V L H M I Y M R A L Q I V Y G I R   GRIIP
 31  L S K S D F L P N P K P E V L Y M I Y M R A L Q L V Y G V R   HW051

 61  L E H F Y M M P V N S E V M Y P H L M E G F L P F S N L V T   GRIIP
 61  L E H F Y M M P V N I E V M Y P H I M E G F L P V S N L F F   HW051

 91  H L D S F L P I C R V N D F E T A D I L C P K A K R T S R F   GRIIP
 91  H L D S F M P I C R V N D F E I A D I L Y P K A N R T S R F   HW051

121  L S G I I N F I H F R E A C R E T Y M E F L W Q Y K S S A D   GRIIP
121  L S G I I N F I H F R E T C L E K Y E E F L Q N K S S V D   HW051

151  K M Q Q L N A A H Q E A L M K L E R L D S V P V E E Q E E F   GRIIP
151  K I Q Q L S N A H Q E A L M K L E K L N S V P V E E Q E E F   HW051

181  K Q L S D G I Q E L Q Q S L N Q D F H Q K T I V L Q E G N S   GRIIP
181  K Q L K D D I Q E L Q H L L N Q D F R Q K T T L Q E R Y T   HW051

211  Q K K S N I S E K T K R L N E L K L S V V S L K E I Q E S L   GRIIP
211  K M K S D F S E K T K H V N E L K L S V V S L K E V Q D S L   HW051
```

FIGURE 2A

FIGURE 2B

241 KTKIVDSPEKLKNYKEKMKDTVQKLKNARQ GRIIP
241 KSKIVDSPEKLKNYKEKMKDTVQKLRSARE HW051

271 EVVEKYEIYGDSVDCLPSCQLEVQLYQKKI GRIIP
271 EVMEKYDIYRDSVDCLPSCQLEVQLYQKKS HW051

301 QDLSDNREKLASILKESLNLEDQIESDESE GRIIP
301 QDLADNREKLSSILKESLNLEGQIDSDSSE HW051

331 LKKLKTEENSFKRLMIVKKEKLATAQFKIN GRIIP
331 LKKLKTEENSLIRLMTLKKERLATMQFKIN HW051

361 KKHEDVKQYKRTVIEDCNKVQEKRGAVYER GRIIP
361 KKQEDVKQYKRTMIEDCNKVQEKRDAVCEQ HW051

391 VTTINQEIQKIKLGIQQLKDAAEREKLKSQ GRIIP
391 VTAINQDIHKIKSGIQQLRDAEKREKLKSQ HW051

421 EIFLNLKTALEKYHDGIEKAAEDSYAKIDE GRIIP
421 EILVDLKSALEKYHEGIEKTTEECCTRIGG HW051

451 KTAELKRKMFKMST GRIIP
451 KTAELKRRMFKMPP HW051

Tissue Category	Clone Count	Found in	Ab Abund	Pct Abund
Cardiovascular System	266190	4/68	4	0.0015
Connective Tissue	144645	1/47	2	0.0014
Digestive System	501101	3/148	4	0.0008
Embryonic Structures	106713	2/21	2	0.0019
Endocrine System	225386	1/53	1	0.0004
Exocrine Glands	254635	2/64	2	0.0008
Genitalia, Female	427284	3/106	3	0.0007
Genitalia, Male	448207	2/114	6	0.0013
Germ Cells	38282	1/5	1	0.0026
Hemic and Immune System	680277	15/159	20	0.0029
Liver	109378	0/35	0	0.0000
Musculoskeletal System	159280	0/47	0	0.0000
Nervous System	955753	2/19	2	0.0002
Pancreas	110207	1/24	1	0.0009
Respiratory System	390086	4/93	5	0.0013
Sense Organs	19256	1/8	1	0.0052
Skin	72292	0/15	0	0.0000
Stomatognathic System	12923	0/10	0	0.0000
Unclassified/Mixed	120926	3/13	5	0.0041
Urinary Tract	279062	2/64	2	0.0007
Totals	5321883	47/1292	6	0.0000

FIGURE 3A

Found in:

Library ID	Clone Count	Library Description	Ab Abund	Pct Abund
BMARTXR02	682	bone marrow tumor line, neuroblastoma, t/6-OHDA,	1	0.1466
TLYMUNT01	3669	T-lymphocytes, allogenic, 40-50M, untreated	3	0.0818
TBLYNOT01	3119	T-B lymphoblast line, leukemia, untreated	2	0.0641
U937NOT01	2067	monocyte line, histiocytic lymphoma, untreated	1	0.0484
BMARTXT03	2162	bone marrow tumor line, neuroblastoma, t/6-OHDA,	1	0.0463
BMARTXT06	2787	bone marrow tumor line, neuroblastoma, untreated	1	0.0359
SPLNTUT02	3017	spleen tumor, Hodgkin's, 45M	1	0.0331
MCLDTXT04	3310	UCB, derived dendritic cells, t/PMA, Ionomycin	1	0.0302
THYMFET03	3577	thymus, fetal, M	1	0.0280
MYEPTXT01	3944	CML precursor line, K-562, 53F, t/5AZA 72 h	1	0.0254
SPLNFET02	7859	spleen, fetal, 23wM	1	0.0127
TLYMNOT08	9784	T-lymphocytes, allogenic anergic, t/OKT3 3 day	1	0.0102

Two pooled libraries, two normalized libraries, and one subtracted library are not shown.
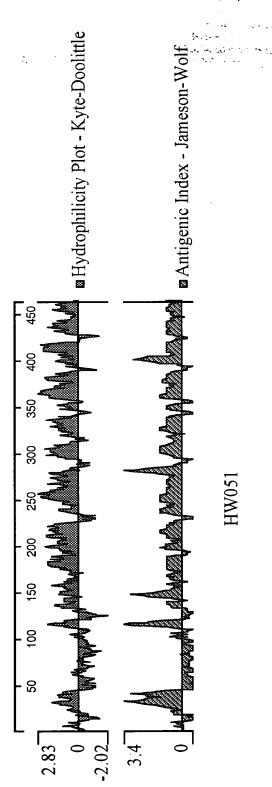
FIGURE 3B

FIGURE 4